

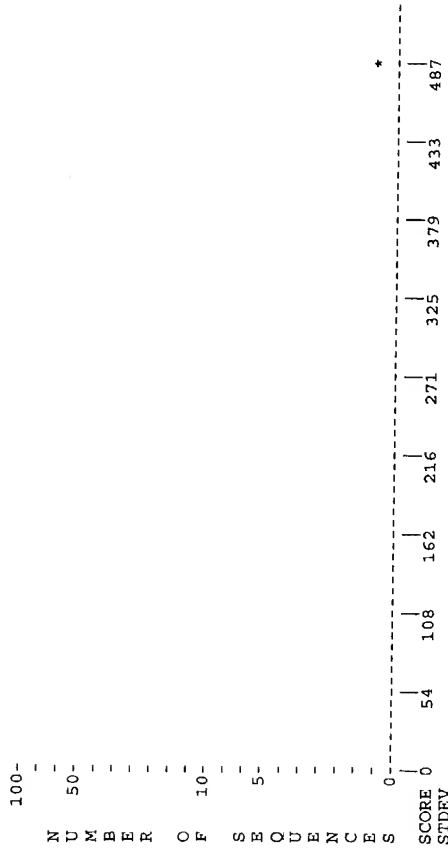
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 069434_4_x_m33987.res made by spaula on Wed 22 Sep 104 12:47:50-PST.

Query sequence being compared: US-10-069-434-4 (1-911)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-069-434-4 (1-911) with:
File : m33987.seq



PARAMETERS

Similarity matrix Unitary
Mismatch penalty 1
Gap penalty 1.00
Gap size penalty 0.33
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 487 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 2785
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Init. Opt. Frame
1. m33987 TOIG of: m33987 check: 7224 2785 487 558 0.00 0

1. US-10-069-434-4 (1-911)
m33987 TOIG of: m33987 check: 7224 from: 1 to: 2785

TOIG of: m33987 check: 7224 from: 1 to: 2785

LOCUS HUMCAIX 2785 bp mRNA linear PRI 31-OCT-1994
DEFINITION Human carbonic anhydrase I (CAI) mRNA, complete cds.
ACCESSION M33987
VERSION M33987.1 GI:179792
KEYWORDS carbonic anhydrase I.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2785)
Lower.N., Brady.H.J., Barlow.J.H., Sowden.J.C., Edwards.M. and
Butterworth.P.H.
TITLE Structure and methylation patterns of the gene encoding human
carbonic anhydrase I
JOURNAL Gene 93 (2), 277-283 (1990)
MEDLINE 91033039
PubMed 2121614
COMMENT Original source text: Human EBV transformed SH B cell line DNA, and
cDNA to mRNA.
Since no intron sequences were provided this entry is treated as if
originating from an mRNA.
Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted
by N.Lowe, 09-MAY-1990.
Author address: N.Lowe
Department of Biochemistry
University College London
Gower Street, London
WC1E 6BT, U.K.
E-mail: UCBMWAR@EUC.LID.UCL.AC.UK@CUNYVM.CUNY.EDU.

FEATURES

Source
1..2785
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="8q13-q22"
1..2785
/gene="CA1"
874..879
/gene="CA1"
902..2165
/gene="CA1"
/note="carbonic anhydrase I mRNA (alt.)"
902..1939
/gene="CA1"
/note="carbonic anhydrase I mRNA (alt.)"
1048..1833
/gene="CA1"
/note="carbonic anhydrase I (EC 4.2.1.1)"
/codon_start=1
/protein_id="AA51910.1"
/db_xref="GI:179793"
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/translation="MASPDWGDYDKNQPEWSKLYPIANGNNSQSPVDIKTSETKHDTS
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EHGSEHTVDGVKYSAEHLVAHWNSAKYSSLAARAKADGLAVIGLVKVGANPKLQK
VLDALQAIKTKGKAPTNFDPSTLLPSSLDFTWYPSGLTHPPYESTVTWICKESIS
VSSQLAQFRSLLSNVEGDNAVPMQHNRRPTQPLKGRTRASF"

ORIGIN

M33987 Length: 2785 September 22, 2004 12:44 Type: N Check: 7224

730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800

TTGTSCACAGCGGAGGTGAAGCAGCAGCGCTTTCTGTGTATAGTCTCAC-TCTGTC--ACCCA--GGCTGGG

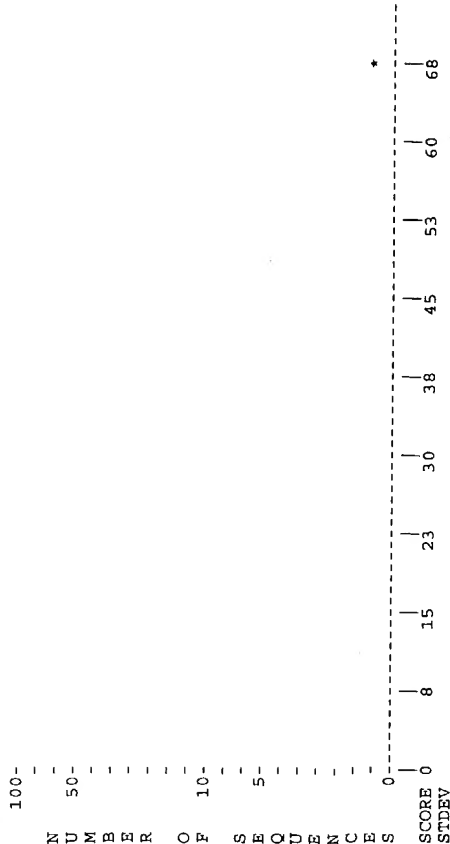
>O<
IntelliGenetics
>O<

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 069434_4_x_m33987_inv.res made by spaula on Wed 22 Sep 104 12:49:06-PST.

Query sequence being compared:US-10-069-434-4' (1-911)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-069-434-4' (1-911) with:
File : m33987.seq



PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 1.00 Window size 500
Gap size penalty 0.33
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
68 0 0.00
Times: CPU 00:00:00.00 Total Elapsed
00:00:00.00

Number of residues: 2785
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

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Sequence Name Description Length Score Score Init. Opt.
1. m33987 TOIG of: m33987 check: 7224 from: 1 to: 2785 68 410 0.00 0

US-10-069-434-4' (1-911)
TOIG of: m33987 check: 7224 from: 1 to: 2785

TOIG of: m33987 check: 7224 from: 1 to: 2785

LOCUS HUMCAIX 2785 bp mRNA linear PRI 31-OCT-1994
DEFINITION Human carbonic anhydrase I (CAI) mRNA, complete cds.

ACCESSION M33987

VERSION M33987.1 GI:179792

KEYWORDS carbonic anhydrase I.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2785)

LOWE,N., Brady,H.J., Barlow,J.H., Sowden,J.C., Edwards,M. and
Butterworth,P.H.

Structure and methylation patterns of the gene encoding human
carbonic anhydrase I

Gene 93 (2), 277-283 (1990)

JOURNAL 91033039

MEDLINE 2121614

PUBMED

COMMENT

Original source text: Human EBV transformed SH B cell line DNA, and
cDNA to mRNA.

Since no intron sequences were provided this entry is treated as if
originating from an mRNA.

Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted

by N.Lowe, 09-MAY-1990.

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FEATURES

Source

1. .2785

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/map="8q13-q22"

1. .2785

/gene="CA1"

874. .879

/gene="CA1"

902. .2165

/gene="CA1"

/note="carbonic anhydrase I mRNA (alt.)"

902. .1939

/gene="CA1"

/note="carbonic anhydrase I mRNA (alt.)"

1048. .1833

/gene="CA1"

/note="carbonic anhydrase I (EC 4.2.1.1)"

/codon_start=1

/protein_id="AA51910.1"

/db_xref="GI:1797933"

/db_xref="GDB:G00-119-047"

/translation="MASPDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSEKHDTS
LKPIVSYNPATAKEIINVGHSHFVNFDNDRSVLKGPFSDSVRLFQHFHGWSTN
EHGSEHTVDGVKYSALHVAHWNSAKYSSLAASKADGLAVIGLVKVGEPKLOK
VLDALQAIKTKGRAPFTNPDPSLTLLPSSLOFWYFGSLTHPPLESVTWICKRESIS
VSSQOLAQFRSLLSNVEGDNAVPMQHNRRPTQPLKGRVTRASF"

ORIGIN

M33987 Length: 2785 September 22, 2004 12:44 Type: N Check: 7224 ..

Initial Score = 68 Optimized Score = 410 Significance = 0.00
Residue Identity = 50% Matches = 535 Mismatches = 329
Gaps = 201 Conservative Substitutions = 0

670 680 690 700 710 720 730
CAGTTTCCTCTCTTGAGCAGCTGATTAAATCCACACCCCAACCACTTCCCTTATCAGGTTCTCACACTCTGG
X
TTTTTC--CCCTGGCATT--TGG
740 750 760 770 780 790 800
GAAAAAGTCAAG---CCAGTGGTTCAGAGCTCTGAGGCTGAGGTGGGAGGATCA---CTTGAGTCCAGGAGTT
GGCCACT-ATGTACCACCT-CTAATCCACACAGGCGCCAGACATCAGACAAATTAAAGACAGCGCCCATGCCCC
710 720 730 740 750 760 770 780 790 800
GAGGAGTGC---AAATTAGCAAGATTGTACCACTGCCCTCCAGCTGGGTGACAGAGTGAGACTCTAT--CA
AAAGCCGCAAAATATGCAA-ATTAT--TCAAAATATTCAACCTAGCTAAC---CCACACCTTTTTCGTG
810 820 830 840 850 860 870
CAGAAAAGCTGTGCTTCAACCTCC--GC-TGTG-----CA-----CAGGAG--AC-----TGC---GAAATTT
TACATAAGCTGCCATTCCTCCCTCCAGCTGTGGTACCCAGCTCCTCAGGTGCAACCCCTGGGTGGTCTCT
880 890 900 910 920 930 940
G-GCCAGC-----TGTGAGAGCTGATGT--TTATAGTGTGCTTTAAACAA-----TCCATGTGACA
210 220 230 240 250
GTGGCAGCCTTCTCTCATTCAGAGCTGTTTCCACAGAGGTAG--TGAAAGAACTGGATTTTCAAGT--TCA
950 960 970 980 990 1000 1010
260 270 280 290 300 310 320
CTCT--CAAGAAGAGTGGAACTGTAAG-AGAACCAGGAT-ATGTCCAGTAGTCCCAAGGATGGTG-GAAGCAG
CITTTGCAAG-AGAAAAGAAACTCAGTAGAA---GATAATGGCAAGT---CCAGACTGGGGATATGATG
1020 1030 1040 1050 1060 1070
330 340 350 360 370 380 390
AGACAAATAGTCAAAATTTGTGAATCGAGTTCTTTTACCTTTCTTTTAAATGAA--TCCAAAGTGTGAG-T
ACAAAATGCTCTGAACTGAGCAAG-CTGTAT--CCCATGTC--CAATGGAATTAACCAATCCCTGTT
1080 1090 1100 1110 1120 1130 1140
400 410 420 430 440 450
AATCTTT--TTGCACT--TGGGAATTAGGTTTCAACATCTGTAA--AAACA-----CTCC--CAAGACAGC--C
GATATTAAACACAGTGAAACCAACATG-ACACTCTCTGAAACCTATTAGTGTCTCTACACACCCAGCCAC
1150 1160 1170 1180 1190 1200 1210
460 470 480 490 500 510
AGTCCATCTGGT--TCA-TGAGTGTGCT-----CA-ACAAAGCTGGGTTATTTGCTGA---ATTCCAGTG
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1220 1230 1240 1250 1260 1270 1280
520 530 540 550 560 570
-AACACATGG-----AGCTCTG--CAGC-ATA-GCTCACTCACTACTATGTGCTCGGAGCCGTGGTCAATCA
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1290 1300 1310 1320 1330 1340 1350
580 590 600 610 620 630
GC--GG-----ACCCCCAGT--GAAGTGG--AA-----CTTCCCGTAACT--GTAGCTTCCAGTGAGAGA
GCATGGTTCAAGAACATACAGTGGTGGAGTCAATATTCTGGCG-AGCTTCAGCTAGCT--CACTG-GAATT
1360 1370 1380 1390 1400 1410 1420
640 650 660 670 680 690
CCACCGCAGAACTGATTTGTTCTCTGTGTCAATCAAG--TCACATT--GAAGGAATGCCGCTGTGCT

CTGCAAAAGTACTCCAGCCTTGCTGAAGCTG-CCTCAAAAGGCTGATGGTTTGGCACTTATTGGTG-TTTTGAT
1430 1440 1450 1460 1470 1480 1490
700 710 720 730 740
GATGATT--TTAG-----CTGAGCTTGGGTCA-TACTTGAT---ACTAAGTGGT---CGGAGGG---
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1500 1510 1520 1530 1540 1550 1560
750 760 770 780 790 800
AAGAGTCATATTCTCTCTCTTGGG-----TTTTTAATCTCAAT--TGA-----GATTGCTGATC--ACCATC
ACGAGCCCCA-TTCACAAATTTTGACCCCTCTACTCTCTCTCTCATCCCTGGATTTCTGGACCTACCT-
1570 1580 1590 1600 1610 1620 1630
810 820 830 840 850 860 870
AGCAATAGGGAATAATTCCTTCAGTGAATAGACCGTGTGCTCGCGTATC-CCCAGCTGAGCCTCGACA
GGCTCT-CTGACTCAT-CCT-CCTCT--TTATGAGAGTGAACCTTGGATCATCTGTGAAGGAGAGCAT---CA
1640 1650 1660 1670 1680 1690
880 890 900 X
TGGTC-CCTCGGGTGGAACTCGAGCCGAAATTCGG
GTGTGAGCTC--AGAGCAGCT--GGCAAAATTCGAGCCTTCTATCAAAATGTTGAAGGTGATAAGCTGTC
1700 1710 1720 1730 1740 1750 1760
CCCATGCGACACA
1770 1780